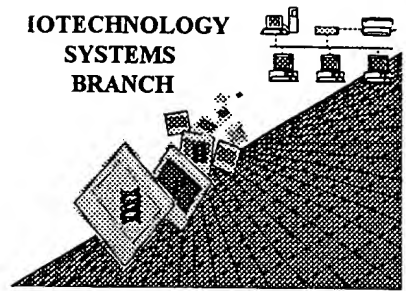


E. O'Hara

# **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/142,471  
Art Unit / Team No. : 1646  
Date Processed by STIC: 1/28/2000

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/142,471

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s) 2 (maybe more). Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(x1) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 f new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

E. O. Hara

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/142,471

DATE: 01/28/2000  
TIME: 11:45:43

Input Set: I142471.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

Does Not Comply  
Corrected Diskette Needed

P.3

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1  <110> APPLICANT: ROEWKAMP, Walter
2      ROSE-JOHN, Stefan
3  <120> TITLE OF INVENTION: CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
4  <130> FILE REFERENCE: 012627-009
5  <140> CURRENT APPLICATION NUMBER: US/09/142,471
6  <141> CURRENT FILING DATE: 1998-11-04
7  <150> EARLIER APPLICATION NUMBER: PCT/DE97/00458
8  <151> EARLIER FILING DATE: 1997-03-07
9  <150> EARLIER APPLICATION NUMBER: DE 196 08 813.5
10 <151> EARLIER FILING DATE: 1996-03-07
11 <160> NUMBER OF SEQ ID NOS: 13
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
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20 <220> FEATURE:
21 <221> NAME/KEY: mat_peptide
22 <222> LOCATION: (91)..(1608)
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (34)..(1608)
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Unknown Organism: A conjugate
28     comprising two polypeptides with a mutual
29     affinity.
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33                                     -15
34     ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg   102
35     Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
36     -10                               -5                               -1    1
37     cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca   150
38     Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu Thr Ser Leu Pro
39     5                               10                               15                               20
40     gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat   198
41     Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn
42     25                               30                               35
43     gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc   246
44     Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala Gly Ser His Pro
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RAW SEQUENCE LISTING  
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47	Ser	Arg	Trp	Ala	Gly	Met	Gly	Arg
48			55			60		
49	ctc	cac	gac	tct	gga	aac	tat	tca
50	Leu	His	Asp	Ser	Gly	Asn	Tyr	Ser
51			70			75		
52	ggg	act	gtg	cac	ttg	ctg	gtg	gat
53	Gly	Thr	Val	His	Leu	Leu	Val	Asp
54			85			90		
55	tcc	tgc	ttc	cgg	aag	agc	ccc	ctc
56	Ser	Cys	Phe	Arg	Lys	Ser	Pro	Leu
57								
58	cct	cgg	agc	acc	cca	tcc	ctg	acg
59	Pro	Arg	Ser	Thr	Pro	Ser	Leu	Thr
60								
61	aag	ttt	cag	aac	agt	ccg	gcc	gaa
62	Lys	Phe	Gln	Asn	Ser	Pro	Ala	Glu
63								
64	tcc	cag	gag	tcc	cag	aag	ttc	tcc
65	Ser	Gln	Glu	Ser	Gln	Lys	Phe	Ser
66								
67	gac	agc	tct	ttc	tac	ata	gtg	tcc
68	Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser
69								
70	agc	aag	ttc	agc	aaa	act	caa	acc
71	Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr
72								
73	cct	gat	ccg	cct	gcc	aac	atc	aca
74	Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr
75								
76	cgc	tgg	ctc	agt	gtc	acc	tgg	caa
77	Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln
78								
79	ttc	tac	aga	cta	cgg	ttt	gag	ctc
80	Phe	Tyr	Arg	Leu	Arg	Phe	Glu	Leu
81								
82	aca	ttc	aca	aca	tgg	atg	gtc	aag
83	Thr	Phe	Thr	Thr	Trp	Met	Val	Lys
84								
85	cac	gac	gcc	tgg	agc	ggc	ctg	agg
86	His	Asp	Ala	Trp	Ser	Gly	Leu	Arg
87								
88	gag	gag	ttc	ggg	caa	ggc	gag	tgg
89	Glu	Glu	Phe	Gly	Gln	Gly	Glu	Trp
90								
91	ggc	acg	cct	tgg	aca	gaa	tcc	agg
92	Gly	Thr	Pro	Trp	Thr	Glu	Ser	Arg
93								
94	ggg	tct	gga	ggg	gga	ggg	tct	gga

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RAW SEQUENCE LISTING  
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97      ccc cca gga gaa gat tcc aaa gat gta gcc gcc cca cac aga cag cca      1110
98      Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro
99      325                               330                               335                               340
100     ctc acc tct tca gaa cga att gac aaa caa att cgg tac atc ctc gac      1158
101     Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp
102      345                               350                               355
103     ggc atc tca gcc ctg aga aag gag aca tgt aac aag agt aac atg tgt      1206
104     Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys
105      360                               365                               370
106     gaa agc agc aaa gag gca ctg gca gaa aac aac ctg aac ctt cca aag      1254
107     Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys
108      375                               380                               385
109     atg gct gaa aaa gat gga tgc ttc caa tct gga ttc aat gag gag act      1302
110     Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr
111      390                               395                               400
112     tgc ctg gtg aaa atc atc act ggt ctt ttg gag ttt gag gta tac cta      1350
113     Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu
114     405                               410                               415                               420
115     gag tac ctc cag aac aga ttt gag agt agt gag gaa caa gcc aga gct      1398
116     Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala
117      425                               430                               435
118     gtg cag atg agt aca aaa gtc ctg atc cag ttc ctg cag aaa aag gca      1446
119     Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala
120      440                               445                               450
121     aag aat cta gat gca ata acc acc cct gac cca acc aca aat gcc agc      1494
122     Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser
123      455                               460                               465
124     ctg ctg acg aag ctg cag gca cag aac cag tgg ctg cag gac atg aca      1542
125     Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr
126      470                               475                               480
127     act cat ctc att ctg cgc agc ttt aag gag ttc ctg cag tcc agc ctg      1590
128     Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu
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130     agg gct ctt cgg caa atg tagcatgggc accgtcgac      1627
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132      505
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135 <212> TYPE: PRT
136 <213> ORGANISM: Unknown
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138     Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
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140     Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
141      -1      1                               5                               10
142     Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
143      15                               20                               25
144     Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys

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*see item 7 on Enn Summary Sheet*

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RAW SEQUENCE LISTING  
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145	30	35	40	45
146	Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg			
147		50	55	60
148	Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys			
149		65	70	75
150	Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val			
151		80	85	90
152	Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser			
153		95	100	105
154	Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr			
155		110	115	120
156	Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp			
157		130	135	140
158	Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys			
159		145	150	155
160	Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met			
161		160	165	170
162	Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe			
163		175	180	185
164	Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val			
165		190	195	200
166	Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp			
167		210	215	220
168	Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg			
169		225	230	235
170	Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp			
171		240	245	250
172	Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His			
173		255	260	265
174	Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser			
175		270	275	280
176	Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser			
177		290	295	300
178	Pro Pro Ala Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly			
179		305	310	315
180	Gly Gly Ser Val Glu Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val			
181		320	325	330
182	Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys			
183		335	340	345
184	Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr			
185		350	355	360
186	Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu			
187		370	375	380
188	Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln			
189		385	390	395
190	Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu			
191		400	405	410
192	Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser			
193		415	420	425
194	Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile			

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/142,471

DATE: 01/28/2000  
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Input Set: I142471.RAW

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195          430          435          440          445
196      Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro
197                      450                      455                      460
198      Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn
199                      465                      470                      475
200      Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys
201                      480                      485                      490
202      Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
203          495          500          505
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207 <213> ORGANISM: Unknown
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214 <220> FEATURE:
215 <221> NAME/KEY: mat_peptide
216 <222> LOCATION: (91)..(1593)
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Description of Unknown Organism:A conjugate
219      comprising two polypeptides with a mutual
220      affinity.
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223                      Met Leu Ala Val Gly Cys Ala
224                      -15
225      ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102
226      Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
227          -10          -5          -1 1
228      cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150
229      Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu Thr Ser Leu Pro
230          5          10          15          20
231      gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198
232      Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn
233          25          30          35
234      gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc 246
235      Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala Gly Ser His Pro
236          40          45          50
237      agc aga tgg gct ggc atg gga agg agg ctg ctg ctg agg tcg gtg cag 294
238      Ser Arg Trp Ala Gly Met Gly Arg Arg Leu Leu Leu Arg Ser Val Gln
239          55          60          65
240      ctc cac gac tct gga aac tat tca tgc tac ccg gcc ggc cgc cca gct 342
241      Leu His Asp Ser Gly Asn Tyr Ser Cys Tyr Arg Ala Gly Arg Pro Ala
242          70          75          80
243      ggg act gtg cac ttg ctg gtg gat gtt ccc ccc gag gag ccc cag ctc 390
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VERIFICATION SUMMARY  
PATENT APPLICATION US/09/142,471

DATE: 01/28/2000  
TIME: 11:45:43

Input Set: I142471.RAW

Line	? Error/Warning	Original Text
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